Fronda

1600

RAW SEQUENCE LISTING   DATE: 08/22/2001
PATENT APPLICATION: US/09/835,381   TIME: 10:33:35

Input Set : A:\ES.txt
Output Set: N:\CRF3\08222001\I835381.raw

ENTERED

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 3 <110> APPLICANT: SUGA, Mikiko
 4         ASAKURA, Yoko
 5         MORI, Yukiko
 6         ITO, Hisao
 7         KURAHASHI, Osamu
 9 <120> TITLE OF INVENTION: ARGININE REPRESSOR DEFICIENT STRAIN OF CORYNEFORM BACTERIUM
AND METHOD
10         FOR PRODUCING L-ARGININE
12 <130> FILE REFERENCE: 206018US0
14 <140> CURRENT APPLICATION NUMBER: 09/835,381
15 <141> CURRENT FILING DATE: 2001-04-17
17 <150> PRIOR APPLICATION NUMBER: JP2000-129167
18 <151> PRIOR FILING DATE: 2000-04-28
20 <160> NUMBER OF SEQ ID NOS: 22
22 <170> SOFTWARE: PatentIn version 3.1
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26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: synthetic DNA
32 <400> SEQUENCE: 1
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37 <211> LENGTH: 30
38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: synthetic DNA
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48 <210> SEQ ID NO: 3
49 <211> LENGTH: 26
50 <212> TYPE: DNA
51 <213> ORGANISM: Artificial Sequence
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54 <223> OTHER INFORMATION: synthetic DNA
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62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: synthetic DNA
68 <400> SEQUENCE: 4
69 aggccttttt ttaaggcagt tattg                                  25
72 <210> SEQ ID NO: 5
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73 <211> LENGTH: 4447
74 <212> TYPE: DNA
75 <213> ORGANISM: Brevibacterium lactofermentum
77 <220> FEATURE:
78 <221> NAME/KEY: CDS
79 <222> LOCATION: (1318)..(2598)
80 <223> OTHER INFORMATION:
83 <400> SEQUENCE: 5
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86 ttttccctcg tttgcccact ttttaatggt ggccggggtg agagctacgc gggcggcgac   120
88 ctgctgcgct gtgatccaat attcggggtc gttcactggt tccccttttct gatttctggc   180
90 atagaagaac ccccgtgaac tgtgtggttc cgggggttgc tgatttttgc gagacttctc   240
92 gcgcaattcc ctagcttagg tgaaaacacc atgaaacact agggaaacac ccatgaaaca   300
94 cccattaggg cagtagggcg gcttcttcgt ctagggcttg catttgggcg gtgatctggt   360
96 ctttagcgtg tgaaagtgtg tcgtaggtgg cgtgctcaat gcactcgaac gtcacgtcat   420
98 ttaccgggtc acggtgggca aagagaacta gtgggttaga cattgttttc ctcgttgtcg   480
100 gtggtggtga gcttttctag ccgctcggta aacgcggcga tcatgaactc ttggaggttt   540
102 tcaccgttct gcatgcctgc gcgcttcatg tcctcacgta gtgccaaagg aacgcgtgcg   600
104 gtgaccacga cgggcttagc ctttgcctgc gcttctagtg cttcgatggt ggcttgtgcc   660
106 tgcgcttgct gcgcctgtag tgcctgttga gcttcttgta gttgctgttc tagctgtgcc   720
108 ttggttgcca tgctttaaga ctctagtagc tttcctgcga tatgtcatgc gcatgcgtag   780
110 caaacattgt cctgcaactc attcattatg tgcagtgctc ctgttactag tcgtacatac   840
112 tcatatttac ctagtctgca tgcagtgcat gcacatgcag tcatgtcgtg ctaatgtgta   900
114 aaacatgtac atgcagattg ctgggggtgc aggggcgga gccaccctgt ccatgcgggg   960
116 tgtggggctt gccccgccgg tacagacagt gagcaccggg gcacctagtc gcggataccc   1020
118 cccctaggta tcggacacgt aaccctccca tgtcgatgca aatctttaac attgagtacg   1080
120 ggtaagctgg cacgcatagc caagctaggc ggccaccaaa caccactaaa aattaatagt   1140
122 ccctagacaa gacaaacccc cgtgcgagct accaactcat atgcacgggg gccacataac   1200
124 ccgaaggggt ttcaattgac aaccatagca ctagctaaga caacgggcac aacacccgca   1260
126 caaactcgca ctgcgcaacc ccgcacaaca tcgggtctag gtaacactga aatagaa      1317
128 gtg aac acc tct aag gaa ccg cag gtc aat gag ggt tct aag gtc act   1365
129 Val Asn Thr Ser Lys Glu Pro Gln Val Asn Glu Gly Ser Lys Val Thr
130 1                5                   10                  15
132 cgc gct agg gcg tgg cgt agg caa aac gtc atg tac aag atc acc aat   1413
133 Arg Ala Arg Ala Trp Arg Arg Gln Asn Val Met Tyr Lys Ile Thr Asn
134         20                  25                  30
136 agt aag gct ctg gcg ggg tgc cat agg tgg cgc agg gac gaa gct gtt   1461
137 Ser Lys Ala Leu Ala Gly Cys His Arg Trp Arg Arg Asp Glu Ala Val
138         35                  40                  45
140 gcg gtg tcc tgg tcg tct aac ggt gct tcg cag ttt gag ggt ctg caa   1509
141 Ala Val Ser Trp Ser Ser Asn Gly Ala Ser Gln Phe Glu Gly Leu Gln
142         50                  55                  60
144 aac tct cac tct cgc tgg ggg tca cct ctg gct gaa ttg gaa gtc atg   1557
145 Asn Ser His Ser Arg Trp Gly Ser Pro Leu Ala Glu Leu Glu Val Met
146 65                  70                  75                  80
148 ggc gaa cgc cgc att gag ctg gct att gct act aag aat cac ttg gcg   1605
149 Gly Glu Arg Arg Ile Glu Leu Ala Ile Ala Thr Lys Asn His Leu Ala
150         85                  90                  95
152 gcg ggt ggc gcg ctc atg atg ttt gtg ggc act gtt cga cac aac cgc   1653
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153 Ala Gly Gly Ala Leu Met Met Phe Val Gly Thr Val Arg His Asn Arg
154             100                 105                 110
156 tca cag tca ttt gcg cag gtt gaa gcg ggt att aag act gcg tac tct     1701
157 Ser Gln Ser Phe Ala Gln Val Glu Ala Gly Ile Lys Thr Ala Tyr Ser
158         115                 120                 125
160 tcg atg gtg aaa aca tct cag tgg aag aaa gaa cgt gca cgg tac ggg     1749
161 Ser Met Val Lys Thr Ser Gln Trp Lys Lys Glu Arg Ala Arg Tyr Gly
162     130                 135                 140
164 gtg gag cac acc tat agt gac tat gag gtc aca gac tct tgg gcg aac     1797
165 Val Glu His Thr Tyr Ser Asp Tyr Glu Val Thr Asp Ser Trp Ala Asn
166 145                 150                 155                 160
168 ggt tgg cac ttg cac cgc aac atg ctg ttg ttc ttg gat cgt cca ctg     1845
169 Gly Trp His Leu His Arg Asn Met Leu Leu Phe Leu Asp Arg Pro Leu
170                 165                 170                 175
172 tct gac gat gaa ctc aag gcg ttt gag gat tcc atg ttt tcc cgc tgg     1893
173 Ser Asp Asp Glu Leu Lys Ala Phe Glu Asp Ser Met Phe Ser Arg Trp
174             180                 185                 190
176 tct gct ggt gtg gtt aag gcc ggt atg gac gcg cca ctg cgt gag cac     1941
177 Ser Ala Gly Val Val Lys Ala Gly Met Asp Ala Pro Leu Arg Glu His
178         195                 200                 205
180 ggg gtc aaa ctt gat cag gtg tct acc tgg ggt gga gac gct gcg aaa     1989
181 Gly Val Lys Leu Asp Gln Val Ser Thr Trp Gly Gly Asp Ala Ala Lys
182     210                 215                 220
184 atg gca acc tac ctc gct aag ggc atg tct cag gaa ctg act ggc tcc     2037
185 Met Ala Thr Tyr Leu Ala Lys Gly Met Ser Gln Glu Leu Thr Gly Ser
186 225                 230                 235                 240
188 gct act aaa acc gcg tct aag ggg tcg tac acg ccg ttt cag atg ttg     2085
189 Ala Thr Lys Thr Ala Ser Lys Gly Ser Tyr Thr Pro Phe Gln Met Leu
190                 245                 250                 255
192 gat atg ttg gcc gat caa agc gac gcc ggc gag gat atg gac gct gtt     2133
193 Asp Met Leu Ala Asp Gln Ser Asp Ala Gly Glu Asp Met Asp Ala Val
194             260                 265                 270
196 ttg gtg gct cgg tgg cgt gag tat gag gtt ggt tct aaa aac ctg cgt     2181
197 Leu Val Ala Arg Trp Arg Glu Tyr Glu Val Gly Ser Lys Asn Leu Arg
198         275                 280                 285
200 tcg tcc tgg tca cgt ggg gct aag cgt gct ttg ggc att gat tac ata     2229
201 Ser Ser Trp Ser Arg Gly Ala Lys Arg Ala Leu Gly Ile Asp Tyr Ile
202     290                 295                 300
204 gac gct gat gta cgt cgt gaa atg gaa gaa gaa ctg tac aag ctc gcc     2277
205 Asp Ala Asp Val Arg Arg Glu Met Glu Glu Glu Leu Tyr Lys Leu Ala
206 305                 310                 315                 320
208 ggt ctg gaa gca ccg gaa cgg gtc gaa tca acc cgc gtt gct gtt gct     2325
209 Gly Leu Glu Ala Pro Glu Arg Val Glu Ser Thr Arg Val Ala Val Ala
210                 325                 330                 335
212 ttg gtg aag ccc gat gat tgg aaa ctg att cag tct gat ttc gcg gtt     2373
213 Leu Val Lys Pro Asp Asp Trp Lys Leu Ile Gln Ser Asp Phe Ala Val
214                 340                 345                 350
216 agg cag tac gtt cta gat tgc gtg gat aag gct aag gac gtg gcc gct     2421
217 Arg Gln Tyr Val Leu Asp Cys Val Asp Lys Ala Lys Asp Val Ala Ala
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218         355                   360                   365
220 gcg caa cgt gtc gct aat gag gtg ctg gca agt ctg ggt gtg gat tcc    2469
221 Ala Gln Arg Val Ala Asn Glu Val Leu Ala Ser Leu Gly Val Asp Ser
222     370                   375                   380
224 acc ccg tgc atg atc gtt atg gat gat gtg gac ttg gac gcg gtt ctg    2517
225 Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu
226 385                   390                   395                   400
228 cct act cat ggg gac gct act aag cgt gat ctg aat gcg gcg gtg ttc    2565
229 Pro Thr His Gly Asp Ala Thr Lys Arg Asp Leu Asn Ala Ala Val Phe
230               405                   410                   415
232 gcg ggt aat gag cag act att ctt cgc acc cac taaaagcggc ataaaccccg  2618
233 Ala Gly Asn Glu Gln Thr Ile Leu Arg Thr His
234               420                   425
236 ttcgatattt tgtgcgatga atttatggtc aatgtcgcgg gggcaaacta tgatgggtct  2678
238 tgttgttgac aatggctgat ttcatcagga atggaactgt catgctgtta tgtgcctggc  2738
240 tcctaatcaa agctggggac aatgggttgc cccgttgatc tgatctagtt cggattggcg  2798
242 gggcttcact gtatctgggg gtggcatcgt gaatagattg cacaccgtag tgggcagtgt  2858
244 gcacaccata gtgggcatga gtaataccta cgcgcgcgtg ggctagggct taacgcgcgt  2918
246 tttgccgtgc tgcggggcat acgttagcgc atacgctttt ttctgtgaaa ccttttttgtg 2978
248 ttgttgtttc gtgttggttt cctttctgtt ggcgggggcaa cttaacgcct gcgggggtgg   3038
250 ttgttgacgt taacggggggt agttttttatt cccctagtgg tttttcagta cgacaatcga  3098
252 gaaagacctg tttcagccag ttcgggtcat gttcgtcggt atggccacgt gcatagcgac  3158
254 cagttttcga gttcactggg attttttggtg catcgaacaa gatgtaggac aatgcggttt  3218
256 ctaggtctac ttttttgcttt atgccgtaca agccccgtgg gtattcagcg attgattcca  3278
258 aggcggcttc ccagtcctgt tttgtgaagg actggcttag ttctaggtct gtgtctgggt  3338
260 agtactgctt gtttgtgtaa gcgccgttgg tgctcattga tgattccttt gaagtgtttg  3398
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264 tatgaggtcg gctaggtagg tttccggggt gcctaggttg cgtaggtcta gcaaatcccg  3518
266 gtatgtggcc tgtgcgctgc gctggtggtg catacagtcg ttaagctggg ctttttacgtc  3578
268 tgcgatgcgg tggcggttag gcatgttggt gtgcttcttc caagtactca cgggcgggtt  3638
270 ttgtgtatgc ctggcgtgat gcttctttga gctgttggag ttccgcttgg agtgcgggta  3698
272 gttcgtccgc gaactgcttg tggtactcgt atttctcttg ttcctgggcg atagcatttg  3758
274 cgttgaattg cagggcggtg agttcgtcca cgcgtcgttt tgctgcgttg gtcatggtgg  3818
276 cgtgccattt gcggttgtgg acgcggggtt caaggttgcg cacggctgct tcggctaggt  3878
278 tggtggctgc tttttttcagt gctcgggctt cccgttcctc gtccaacgag agcacctttg  3938
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282 gggagaggtc gtttttcacg atgcgtcgaa tgtggtcgtt gtgggtgctg agttggtgtg  4058
284 agaggtagtg gggttctggg atttcggcga gttggtcgag gttggtgtag tgcgggttgc  4118
286 ggcctggttg gttgggttcg ctggggaggt cgatgtatcc ggttgagtct ccggcgtggt  4178
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292 cggggagaat gttctttttgg gtcatggctt ctctttctgt tgctctgtaa gtccgtatgt  4358
294 gggcatggga aagcccccggc aacccctttgg gtcaaccggg gctagatagt cgcttagaat  4418
296 ggcttctagg ctgcgtctcg gggtgtggc                                      4447
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300 <211> LENGTH: 427
301 <212> TYPE: PRT
302 <213> ORGANISM: Brevibacterium lactofermentum
304 <400> SEQUENCE: 6
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306 Val Asn Thr Ser Lys Glu Pro Gln Val Asn Glu Gly Ser Lys Val Thr
307 1             5                 10              15
310 Arg Ala Arg Ala Trp Arg Arg Gln Asn Val Met Tyr Lys Ile Thr Asn
311         20                  25                  30
314 Ser Lys Ala Leu Ala Gly Cys His Arg Trp Arg Arg Asp Glu Ala Val
315         35                  40                  45
318 Ala Val Ser Trp Ser Ser Asn Gly Ala Ser Gln Phe Glu Gly Leu Gln
319         50                  55                  60
322 Asn Ser His Ser Arg Trp Gly Ser Pro Leu Ala Glu Leu Glu Val Met
323 65                  70                  75                  80
326 Gly Glu Arg Arg Ile Glu Leu Ala Ile Ala Thr Lys Asn His Leu Ala
327                 85                  90                  95
330 Ala Gly Gly Ala Leu Met Met Phe Val Gly Thr Val Arg His Asn Arg
331             100                 105                 110
334 Ser Gln Ser Phe Ala Gln Val Glu Ala Gly Ile Lys Thr Ala Tyr Ser
335         115                 120                 125
338 Ser Met Val Lys Thr Ser Gln Trp Lys Lys Glu Arg Ala Arg Tyr Gly
339         130                 135                 140
342 Val Glu His Thr Tyr Ser Asp Tyr Glu Val Thr Asp Ser Trp Ala Asn
343 145             150                 155                 160
346 Gly Trp His Leu His Arg Asn Met Leu Leu Phe Leu Asp Arg Pro Leu
347                 165                 170                 175
350 Ser Asp Asp Glu Leu Lys Ala Phe Glu Asp Ser Met Phe Ser Arg Trp
351             180                 185                 190
354 Ser Ala Gly Val Val Lys Ala Gly Met Asp Ala Pro Leu Arg Glu His
355         195                 200                 205
358 Gly Val Lys Leu Asp Gln Val Ser Thr Trp Gly Gly Asp Ala Ala Lys
359         210                 215                 220
362 Met Ala Thr Tyr Leu Ala Lys Gly Met Ser Gln Glu Leu Thr Gly Ser
363 225                 230                 235                 240
366 Ala Thr Lys Thr Ala Ser Lys Gly Ser Tyr Thr Pro Phe Gln Met Leu
367                 245                 250                 255
370 Asp Met Leu Ala Asp Gln Ser Asp Ala Gly Glu Asp Met Asp Ala Val
371             260                 265                 270
374 Leu Val Ala Arg Trp Arg Glu Tyr Glu Val Gly Ser Lys Asn Leu Arg
375         275                 280                 285
378 Ser Ser Trp Ser Arg Gly Ala Lys Arg Ala Leu Gly Ile Asp Tyr Ile
379         290                 295                 300
382 Asp Ala Asp Val Arg Arg Glu Met Glu Glu Glu Leu Tyr Lys Leu Ala
383 305                 310                 315                 320
386 Gly Leu Glu Ala Pro Glu Arg Val Glu Ser Thr Arg Val Ala Val Ala
387             325                 330                 335
390 Leu Val Lys Pro Asp Asp Trp Lys Leu Ile Gln Ser Asp Phe Ala Val
391         340                 345                 350
394 Arg Gln Tyr Val Leu Asp Cys Val Asp Lys Ala Lys Asp Val Ala Ala
395         355                 360                 365
398 Ala Gln Arg Val Ala Asn Glu Val Leu Ala Ser Leu Gly Val Asp Ser
399         370                 375                 380
402 Thr Pro Cys Met Ile Val Met Asp Asp Val Asp Leu Asp Ala Val Leu
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/835,381

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